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#3

SEQUENCE LISTING

<110> GORING, Daphne R. et al.

<120> PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES

<130> P 25,762 USA

<140> US 10/069,304

<141> 2002-02-19

<150> PCT/CA00/00966

<151> 2000-08-18

<150> US 60/149,466

<151> 1999-08-19

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<151> 1999-10-13

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<170> PatentIn Ver. 2.1

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Leu 615	Tyr	Pro	Ser	Gly	Ser 620	Ser	Ser	Glu	Gly	Gln 625	Thr	Thr	Arg	Glu	Met 630	

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 Arg Glu Gly Gly Ser Pro Arg Pro Pro Ser Ser Pro Ser Pro Pro Ser
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 Gly Gly Val Ala Leu Leu Val Ile Val Thr Leu Ile Cys Leu Leu Cys
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 Pro Pro Pro Pro Gly Pro Lys Ala Gly Gly Pro Tyr Gly Gly Gln Gln
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 Gln Gln Trp Arg Gln Gln Asn Ala Thr Pro Pro Ser Asp His Val Val
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 Tyr Ser Asp Arg Pro Val Leu Pro Pro Pro Ser Pro Gly Leu Val Leu
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 Gly Phe Ser Lys Ser Thr Phe Thr Tyr Glu Glu Leu Ala Arg Ala Thr
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 Val His Lys Gly Val Leu Pro Ser Gly Lys Glu Val Ala Val Lys Gln
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Glu	Ile	Ile	Ser	Arg	Val	His	His	Arg	His	Leu	Val	Ser	Leu	Val	Gly
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Tyr	Cys	Ile	Ala	Gly	Ala	Lys	Arg	Leu	Leu	Val	Tyr	Glu	Phe	Val	Pro
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Met	Arg	Pro	Gly	Gln	Ser	Asn	Val	Tyr	Ser	Ser	Tyr	Gly	Gly	Ser	Thr
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 <213> Brassica napus

<400> 5

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 Ser Asp Gly Leu Ser Thr Gly Val Val Val Gly Ile Ala Ile Gly Gly
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 Lys Arg Arg Arg Asp Glu Glu Asp Ala Tyr Tyr Val Pro Pro Pro Pro
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 Pro Pro Gly Pro Lys Ala Gly Gly Pro Tyr Gly Gly Gln Gln Gln Gln
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Asp Arg Pro Val Leu Pro Pro Pro Ser Pro Gly Leu Val Leu Gly Phe
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Phe Ser Glu Ala Asn Leu Leu Gly Gln Gly Gly Phe Gly Tyr Val His
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Lys Gly Val Leu Pro Ser Gly Lys Glu Val Ala Val Lys Gln Leu Lys
325 330 335

Val Gly Ser Gly Gln Gly Glu Arg Glu Phe Gln Ala Glu Val Glu Ile
340 345 350

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355 360 365

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Asn Leu Glu Leu His Leu His Gly Glu Gly Arg Pro Thr Met Glu Trp
385 390 395 400

Ser Thr Arg Leu Lys Ile Ala Leu Gly Ser Ala Lys Gly Leu Ser Tyr
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Leu His Glu Asp Cys Asn Pro Lys Ile Ile His Arg Asp Ile Lys Ala
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Ser Asn Ile Leu Ile Asp Phe Lys Phe Glu Ala Lys Val Ala Asp Phe
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Gly Leu Ala Lys Ile Ala Ser Asp Thr Asn Thr His Val Ser Thr Arg
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Val Met Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr Ala Ala Ser Gly
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gtc Val 385	tat Tyr	aaa Lys	ggt Gly	aca Thr	ttg Leu 390	cag Gln	gat Asp	ggt Gly	aaa Lys	gtt Val 395	gtt Val	gcg Ala	gtt Val	aag Lys	cag Gln 400	1200
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gag Glu	atc Ile	atc Ile	agc Ser 420	cgc Arg	gtt Val	cat His	cat His	cgc Arg 425	cat His	ttg Leu	gtc Val	tct Ser	ctg Leu 430	gtt Val	ggt Gly	1296
tac Tyr	tgc Cys	att Ile 435	tca Ser	gac Asp	cag Gln	cat His	aga Arg 440	ttg Leu	ctt Leu	atc Ile	tat Tyr	gag Glu 445	tat Tyr	gtt Val	tct Ser	1344
aat	caa	acc	ttg	gag	cat	cat	ttg	cat	gag	tgg	tct	aag	aga	gtc	cgg	1392

Asn	Gln	Thr	Leu	Glu	His	His	Leu	His	Glu	Trp	Ser	Lys	Arg	Val	Arg	
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Ile	Ala	Ile	Gly	Ser	Ala	Lys	Gly	Leu	Ala	Tyr	Leu	His	Glu	Asp	Cys	
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His	Pro	Lys	Ile	Ile	His	Arg	Asp	Ile	Lys	Ser	Ala	Asn	Ile	Leu	Leu	
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Asp	Asp	Glu	Tyr	Glu	Ala	Gln	Ala	Ile	Met	Lys	Ser	Ser	Phe	Ser	Leu	
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Asp	Leu	Ser	Glu	Leu	Ile	Asp	Thr	Arg	Leu	Glu	Lys	Arg	Tyr	Val	Glu	
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Ser	Gly	Pro	Lys	Arg	Pro	Arg	Met	Val	Gln	Val	Val	Arg	Ala	Leu	Asp	
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Cys	Asp	Gly	Asp	Ser	Gly	Asp	Ile	Ser	Asn	Gly	Ile	Lys	Ile	Gly	Gln	
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Ser	Thr	Thr	Tyr	Asp	Ser	Gly	Gln	Tyr	Asn	Glu	Asp	Ile	Met	Lys	Phe	
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Arg	Lys	Met	Ala	Phe	Gly	Gly	Asp	Asn	Ser	Val	Glu	Ser	Gly	Leu	Tyr	
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Ser	Gly	Asn	Tyr	Ser	Ala	Lys	Ser	Ser	Ser	Asp	Phe	Ser	Gly	Asn	Glu	
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tct	gag	act	cgg	cct	ttc	aac	aac	cga	cgg	ttc	tga					2196
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<212> PRT

<213> Arabidopsis thaliana

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Pro	Pro	Val	Asp	Ser	Ser	Pro	Pro	Ser	Pro	Pro	Ala	Asp	Ser	Ser	Ser	
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Thr	Pro	Pro	Leu	Ser	Glu	Pro	Ser	Thr	Pro	Pro	Pro	Asp	Ser	Gln	Leu	
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Pro	Pro	Leu	Pro	Ser	Ile	Leu	Pro	Pro	Leu	Thr	Asp	Ser	Pro	Pro	Pro	
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Arg	Asn	Ile	Asp	Ser	Tyr	Asn	His	Ser	Gln	Tyr	Leu	Pro	His	Pro	Asn	
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Pro His His Gln Met Gln Ser Ser Gly Thr Pro Asp Ser Ala Ile Leu				335
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Gly Ser Gly Gln Thr His Phe Ser Tyr Glu Glu Leu Ala Glu Ile Thr				350
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Gln Gly Phe Ala Arg Lys Asn Ile Leu Gly Glu Gly Gly Phe Gly Cys				365
		370		375
Val Tyr Lys Gly Thr Leu Gln Asp Gly Lys Val Val Ala Val Lys Gln				380
385		390		395
Leu Lys Ala Gly Ser Gly Gln Gly Asp Arg Glu Phe Lys Ala Glu Val				400
		405		410
Glu Ile Ile Ser Arg Val His His Arg His Leu Val Ser Leu Val Gly				415
		420		425
Tyr Cys Ile Ser Asp Gln His Arg Leu Leu Ile Tyr Glu Tyr Val Ser				430
		435		440
Asn Gln Thr Leu Glu His His Leu His Glu Trp Ser Lys Arg Val Arg				445
		450		455
Ile Ala Ile Gly Ser Ala Lys Gly Leu Ala Tyr Leu His Glu Asp Cys				460
465		470		475
His Pro Lys Ile Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu				480
		485		490
Asp Asp Glu Tyr Glu Ala Gln Ala Ile Met Lys Ser Ser Phe Ser Leu				495
		500		505
Asn Leu Ser Tyr Asp Cys Lys Val Leu Val Ala Asp Phe Gly Leu Ala				510
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Arg Leu Asn Asp Thr Thr Gln Thr His Val Ser Thr Arg Val Met Gly				525
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Thr Phe Gly Tyr Leu Ala Pro Glu Tyr Ala Ser Ser Gly Lys Leu Thr				540
545		550		555
Asp Arg Ser Asp Val Phe Ser Phe Gly Val Leu Leu Glu Leu Val				560
		565		570
Thr Gly Arg Lys Pro Val Asp Gln Thr Gln Pro Leu Gly Glu Glu Ser				575
		580		585
Leu Val Glu Trp Ala Arg Pro Leu Leu Leu Lys Ala Ile Glu Thr Gly				590
		595		600
Asp Leu Ser Glu Leu Ile Asp Thr Arg Leu Glu Lys Arg Tyr Val Glu				605
		610		615
His Glu Val Phe Arg Met Ile Glu Thr Ala Ala Ala Cys Val Arg His				620
625		630		635
Ser Gly Pro Lys Arg Pro Arg Met Val Gln Val Val Arg Ala Leu Asp				640
		645		650
Cys Asp Gly Asp Ser Gly Asp Ile Ser Asn Gly Ile Lys Ile Gly Gln				655
		660		665
Ser Thr Thr Tyr Asp Ser Gly Gln Tyr Asn Glu Asp Ile Met Lys Phe				670
		675		680
Arg Lys Met Ala Phe Gly Gly Asp Asn Ser Val Glu Ser Gly Leu Tyr				685
		690		695
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 Pro Ser Pro Pro Ser Asn Thr Asn Ser Thr Thr Ser Ser Pro Pro Ala
 20 25 30

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Gln	Tyr	Tyr	Gly	Asn	Asn	Asn	Asn	Asn	Asn	Ala	Ser	Gln	Asn	Tyr	Pro	
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tcc Ser 465	gat Asp	gtt Val	ttc Phe	tct Ser	tac Tyr 470	gga Gly	gtt Val	atg Met	tta Leu	ttg Leu 475	gaa Glu	ctt Leu	ata Ile	act Thr	gga Gly 480	1440
aaa Lys	cga Arg	ccg Pro	gtt Val	gat Asp	aat Asn	agc Ser	atc Ile	acc Thr	atg Met	gac Asp	gac Asp	acc Thr	tta Leu	gta Val	gat Asp	1488

485

490

495

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His Ile Cys Ile Ser His Pro Arg Ile Ile His Arg Asp Ile Lys Ala		415
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	485	490
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Asp Ser Leu Val Asp Trp Ala Arg Pro Leu Cys Leu Lys Ala Ala Gln		510
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<213> Arabidopsis thaliana

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cca Pro	ccg Pro	tct Ser	cct Pro	cac His 100	gtc Val	tca Ser	gct Ala	cct Pro	tcc Ser	ggg Gly 105	tca Ser	ccg Pro	cca Pro 110	tta Leu	ccc Pro	336
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Ser	Phe	Gly	Val	Val	Leu	Leu	Glu	Leu	Ile	Thr	Gly	Arg	Pro	Ser	Ile	580	585	590	
Phe	Ala	Lys	Asp	Ser	Ser	Thr	Asn	Gln	Ser	Leu	Val	Asp	Trp	Ala	Arg	595	600	605	
Pro	Leu	Leu	Thr	Lys	Ala	Ile	Ser	Gly	Glu	Ser	Phe	Asp	Phe	Leu	Val	610	615	620	
Asp	Ser	Arg	Leu	Glu	Lys	Asn	Tyr	Asp	Thr	Thr	Gln	Met	Ala	Asn	Met	625	630	635	640
Ala	Ala	Cys	Ala	Ala	Ala	Cys	Ile	Arg	Gln	Ser	Ala	Trp	Leu	Arg	Pro	645	650	655	
Arg	Met	Ser	Gln	Val	Val	Arg	Ala	Leu	Glu	Gly	Glu	Val	Ala	Leu	Arg	660	665	670	
Lys	Val	Glu	Glu	Thr	Gly	Asn	Ser	Val	Thr	Tyr	Ser	Ser	Ser	Glu	Asn	675	680	685	
Pro	Asn	Asp	Ile	Thr	Pro	Arg	Tyr	Gly	Thr	Asn	Lys	Arg	Arg	Phe	Asp	690	695	700	
Thr	Gly	Ser	Ser	Asp	Gly	Tyr	Thr	Ser	Glu	Tyr	Gly	Val	Asn	Pro	Ser	705	710	715	720
Gln	Ser	Ser	Ser	Glu	His	Gln	Gln	Val	Asn	Thr						725	730		

<210> 18

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(27)

<223> N(1) =i N(2) =i N(3) =T/c/A N(4) =i N(5) =A/T N(6) =T/C
N(7) =A/g

<400> 18

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27

<210> 19

<211> 9

<212> PRT

<213> Brassica napus

<220>

<221> PEPTIDE

<222> (1)..(9)

<223> X(1) =F/Y

<400> 19

Gly Gly Phe Gly Ile Val Xaa Lys Gly
1 5

<210> 20

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(22)

<223> N(1) =i N(2) =i N(3) =T/g N(4) =i N(5) =i N(6) =A/g N(7)
=A/g N(8) =T/c

<400> 20

aanatncnng ccatnccnaa nn

22

<210> 21

<211> 8

<212> PRT

<213> Brassica napus

<400> 21

Asp Phe Gly Met Ala Arg Ile Phe
1 5

<210> 22

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 22

taaccaacaa gagaca

16

<210> 23

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>
 <221> misc_feature
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 <223> N(1) =g/A N(2) =i N(3) =g/A N(4) =T/C N(5) =i N(6) =i N(7)
 =A/g N(8) =I N(9) =A/g N(10) =A/g

<400> 23
 annanттng cnanncnaa ntc 23

<210> 24
 <211> 8
 <212> PRT
 <213> Arabidopsis thaliana

<400> 24
 Asp Phe Gly Leu Ala Lys Leu Leu
 1 5

<210> 25
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 25
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<210> 26
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 <213> Artificial Sequence

<220>
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<210> 27
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

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70	80	90	100	110	120
CATTTGCCTT	TTTGATTAG	ATCCAAAGAA	GCAGACAIGT	CCTCGGCGCC	GTCTCCGGGG
130	140	150	160	170	180
ACTGGTTTCG	CTCCATCTCC	ACCATCAAAC	TCCACAACCA	CCACTCCTCC	TCCAGCTTCC
190	200	210	220	230	240
GCTCCTCCTC	CCACCACACC	TTCTTCTCCT	CCGCCGCCAT	CCACTATTCC	GACATCTCCT
250	260	270	280	290	300
CCTCCTTCTT	CTCGCTCTAC	ACCTTCTGCT	CCTCCTCCAT	CTCCACCAAC	TCCATCTACG
310	320	330	340	350	360
CCGGGATCTC	CACCTCCTCT	TCCTCAGCCG	TCTCCACCCG	CTCCAACCTAC	GCCCGGATCT
370	380	390	400	410	420
CCACCCGCAC	CTGTACTTCC	TCCTACTCGA	AACCCTCCAC	CTTCAGTCCC	AGGACCACCG
430	440	450	460	470	480
TCCAATCCTT	CACGCGAAGG	AGGATCTCCT	CGACCTCCAT	CTTCTCCCTC	GCCGCCGTCT
490	500	510	520	530	540
CCTTCTTCCG	ACGGTTTATC	AACAGGAGTG	GTGGTGGGAA	TCGCCATCGG	AGGAGTCGCT
550	560	570	580	590	600
CTGCTTGTA	TAGTGACTCT	GATTTGTCTC	CTCTGTAAGA	AGAAACGACG	GAGAGACGAA
610	620	630	640	650	660
GAAGATGCTT	ACTATGTTCC	TCCGCCACCT	CCTCCTGGTC	CCAAAGCCGG	AGGACCTTAC
670	680	690	700	710	720
GGTGGACAGC	AGCAACAATG	GCGGCAACAA	AACGCAACAC	CACCGTCAGA	TCATGTCGTG
730	740	750	760	770	780
ACGTCACTAC	CACCACCACC	TAAGGCTCCA	TCTCCACCAC	GGCAACCTCC	TCCACCTCCA
790	800	810	820	830	840
CCACCGCCTT	TCATGAGCAG	CAGCGGCGGC	TCCGACTACT	CGGACCGTCC	AGTTCTTCCT
850	860	870	880	890	900
CCACCGTCTC	CAGGGCTTGT	GTTAGGCTTC	TCCAAAAGCA	CTTTCACATA	CGAGGAGCTA
910	920	930	940	950	960
GCTAGAGCCA	CCPATGGTTT	CTCCGAGGCG	AACTTGTTAG	GACAAGGCGG	GTTCGGTTAC
970	980	990	1000	1010	1020
GTGCACAAAG	GTGTGTTGCC	TAGTGGGAAA	GAAGTTGCTG	TGAAGCAGTT	GAAAGTTGGG
1030	1040	1050	1060	1070	1080
AGTGGTCAGG	GAGAGAGGGA	GTTTCAGGCA	GAGGTTGAGA	TCATCAGCAG	AGTTCACCAC
1090	1100	1110	1120	1130	1140
AGGCATCTGG	TGTCTCTTGT	TGGTTATTGC	ATCGCCGGTG	CCAAAAGATT	GCTTGTCTAT
1150	1160	1170	1180	1190	1200
GAGTTTGTTT	CTAACACAA	TCTCGAGCTT	CACCTCCATG	GCGAGGGACG	GCCTACAATG
1210	1220	1230	1240	1250	1260
GAATGGAGCA	CCAGATTGAA	GATTGCTCTT	GGATCTGCTA	AAGGACTTTC	TTATCTTCAT
1270	1280	1290	1300	1310	1320
GAAGATTGCA	ATCCTAAAAT	CATTACCCGT	GATATCAAGG	CTTCAACAT	ATTGATAGAT
1330	1340	1350	1360	1370	1380
TTCAAGTTTG	AAGCTAAGGT	TGCTGATTTT	GGTCTTGCTA	AGATTGCTTC	TGATACAAAC
1390	1400	1410	1420	1430	1440
ACGCATGTAT	CAACACGTGT	GATGGGAACC	TTTGGGTACT	TGGCTCCGGA	ATACGCTGCA
1450	1460	1470	1480	1490	1500
AGCGGAAAGC	TCACGGAGAA	GTCTGACGTT	TTCTCATTTG	GCGTTGTGCT	TTTGGAGCTC
1510	1520	1530	1540	1550	1560

Figure 1(d) (continued on next page)